



SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Coleman, Roger
Bandman, Olga
Wilde, Craig G.
- (ii) TITLE OF THE INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS
- (iii) NUMBER OF SEQUENCES: 11
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
 - (B) STREET: 3174 Porter Drive
 - (C) CITY: Palo Alto
 - (D) STATE: CA
 - (E) COUNTRY: U.S.
 - (F) ZIP: 94304
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/390,740
 - (B) FILING DATE: February 17, 1995
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Luther, Barbara J.
 - (B) REGISTRATION NUMBER: 33,954
 - (C) REFERENCE/DOCKET NUMBER: PF-0027 US
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 415-855-0555
 - (B) TELEFAX: 415-852-0195

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 291 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
- (B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAGGTCT CCGCAGCACT TCTGTGGCTG CTGCTCATAG CAGCTGCCTT CAGCCCCCAG	60
GGGCTCACTG GGCCAGCTTC TGTCCCAACC ACCTGCTGCT TTAACCTGGC CAATAGGAAG	120
ATACCCCTTC AGCGACTAGA GAGCTACAGG AGAATCACCA GTGGCAAATG TCCCCAGAAA	180
GCTGTGATCT TCAAGACCAA ACTGGCCAAG GATATCTGTG CCGACCCCAA GAAGAAGTGG	240
GTGCAGGATT CCATGAAGTA TCTGGACCAA AAATCTCCAA CTCCAAAGCC A	291

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
- (B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Val	Ser	Ala	Ala	Leu	Leu	Trp	Leu	Leu	Leu	Ile	Ala	Ala	Ala
1					5				10					15	
Phe	Ser	Pro	Gln	Gly	Leu	Thr	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys
					20			25					30		

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Cys Phe Asn Leu Ala Asn Arg Lys Ile Pro Leu Gln Arg Leu Glu Ser
35 40 45
Tyr Arg Arg Ile Thr Ser Gly Lys Cys Pro Gln Lys Ala Val Ile Phe
50 55 60
Lys Thr Lys Leu Ala Lys Asp Ile Cys Ala Asp Pro Lys Lys Lys Trp
65 70 75 80
Val Gln Asp Ser Met Lys Tyr Leu Asp Gln Lys Ser Pro Thr Pro Lys
85 90 95
Pro

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
- (B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCTCAGT CACTGGCTCT GAGCCTCCTT ATCCTGGTTC TGGCCTTTGG CATCCCCAGG	60
ACCCAAGGCA GTGATGGAGG GGCTCAGGAC TGTTGCCTCA AGTACAGCCA AAGGAAGATT	120
CCCGCCAAGG TTGTCCGCAG CTACCGGAAG CAGGAACCAA GCTTAGGCTG CTCCATCCCA	180
GCTATCCTGT TCTTGCCCCG CAAGCGCTCT CAGGCAGAGC TATGTGCAGA CCCAAAGGAG	240
CTCTGGGTGC AGCAGCTGAT GCAGCATCTG GACAAGACAC CATCCCCACA GAAACCAGCC	300
CAGGGCTGCA GGAAGGACAG GGGGGCCTCC AAGACTGGCA AGAAAGGAAA GGGCTCCAAA	360
GGCTGCAAGA GGAAGGACAG GTCACAGACC CCTAAAGGGC CA	402

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Human Pancreas

(B) CLONE: 226152

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Met Ala Gln Ser Leu Ala Leu Ser Leu Leu Ile Leu Val Leu Ala Phe
 1           5           10           15
Gly Ile Pro Arg Thr Gln Gly Ser Asp Gly Gly Ala Gln Asp Cys Cys
          20           25           30
Leu Lys Tyr Ser Gln Arg Lys Ile Pro Ala Lys Val Val Arg Ser Tyr
          35           40           45
Arg Lys Gln Glu Pro Ser Leu Gly Cys Ser Ile Pro Ala Ile Leu Phe
          50           55           60
Leu Pro Arg Lys Arg Ser Gln Ala Glu Leu Cys Ala Asp Pro Lys Glu
65           70           75           80
Leu Trp Val Gln Gln Leu Met Gln His Leu Asp Lys Thr Pro Ser Pro
          85           90           95
Gln Lys Pro Ala Gln Gly Cys Arg Lys Asp Arg Gly Ala Ser Lys Thr
          100          105          110
Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser
          115          120          125
Gln Thr Pro Lys Gly Pro
          130
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 97 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

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Met Lys Val Ser Ala Ala Leu Leu Ala Leu Leu Leu Ile Ala Ala Ala
1 5 10 15
Phe Cys Pro Gln Gly Leu Ala Gln Pro Asp Gly Val Asp Thr Pro Thr
20 25 30
Thr Cys Cys Phe Asn Tyr Ile Asn Arg Lys Ile Pro Arg Gln Arg Leu
35 40 45
Glu Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Ser Lys Pro Ala Val
50 55 60
Ile Phe Lys Thr Lys Arg Ala Lys Gln Val Cys Ala Asp Pro Lys Glu
65 70 75 80
Lys Trp Val Gln Asp Ser Met Lys His Leu Asp Lys Gln Thr Pro Lys
85 90 95
Pro

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MIP-1 α

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala
1 5 10 15
Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala
20 25 30
Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala
35 40 45
Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe
50 55 60
Leu Thr Lys Arg Ser Arg Gln Val Cys Ala Asp Pro Ser Glu Glu Trp
65 70 75 80
Val Gln Lys Tyr Val Ser Asp Leu Glu Leu Ser Ala

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MIP-1 β

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```

Met Lys Leu Cys Val Thr Val Leu Ser Leu Leu Met Leu Val Ala Ala
 1              5              10              15
Phe Cys Ser Pro Ala Leu Ser Ala Pro Met Gly Ser Asp Pro Pro Thr
      20              25              30
Ala Cys Cys Phe Ser Tyr Thr Ala Arg Lys Leu Pro Arg Asn Phe Val
      35              40              45
Val Asp Tyr Tyr Glu Thr Ser Ser Leu Cys Ser Gln Pro Ala Val Val
      50              55              60
Phe Gln Thr Lys Arg Ser Lys Gln Val Cys Ala Asp Pro Ser Glu Ser
65              70              75              80
Trp Val Gln Glu Tyr Val Tyr Asp Leu Glu Leu Asn
      85              90

```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: RANTES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Met Lys Val Ser Ala Ala Arg Leu Ala Val Ile Leu Ile Ala Thr Ala
 1              5              10              15
Leu Cys Ala Pro Ala Ser Ala Ser Pro Tyr Ser Ser Asp Thr Thr Pro
      20              25              30
Cys Cys Phe Ala Tyr Ile Ala Arg Pro Leu Pro Arg Ala His Ile Lys
      35              40              45
Glu Tyr Phe Tyr Thr Ser Gly Lys Cys Ser Asn Pro Ala Val Val Phe
      50              55              60
Val Thr Arg Lys Asn Arg Gln Val Cys Ala Asn Pro Glu Lys Lys Trp
65              70              75              80
Val Arg Glu Tyr Ile Asn Ser Leu Glu Met Ser
      85              90
```

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 99 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: GenBank

(B) CLONE: MCP-1

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
Met Lys Val Ser Ala Ala Leu Leu Cys Leu Leu Leu Ile Ala Ala Thr
 1              5              10              15
Phe Ile Pro Gln Gly Leu Ala Gln Pro Asp Ala Ile Asn Ala Pro Val
```

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```

                20                25                30
Thr Cys Cys Tyr Asn Phe Thr Asn Arg Lys Ile Ser Val Gln Arg Leu
    35                40                45
Ala Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Pro Lys Glu Ala Val
    50                55                60
Ile Phe Lys Thr Ile Val Ala Lys Glu Ile Cys Ala Asp Pro Lys Gln
    65                70                75                80
Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr
                85                90                95
Pro Lys Thr
```

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MCP-2

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```

Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val
 1                5                10                15
Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile
    20                25                30
Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg
    35                40                45
Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser
    50                55                60
Met Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro
    65                70                75
```

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MCP-3

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

```

Met Trp Lys Pro Met Pro Ser Pro Ser Asn Met Lys Ala Ser Ala Ala
 1               5               10               15
Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala Phe Ser Pro Gln Gly Leu
      20               25               30
Ala Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe
      35               40               45
Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr
      50               55               60
Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu
      65               70               75               80
Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe
      85               90               95
Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu
      100               105

```